What is claimed is:

1. A system for designing a probes using heterogeneous genetic information, comprising:

a storage unit storing a crosslink map having records according to the version of a genome sequence;

an information search unit searching for the identifier and sequence information corresponding to target genetic information among the genetic information about the genome sequence in the crosslink map; and

a location estimation unit determining a reference group made up of reference genetic information which is contained in more than a predetermined number in an organism, calculating difference values of the start positions and the end positions of the reference genetic information based on the crosslink map, and determining the location of the target genetic information on the latest genome sequence by a location shift corresponding to the difference values.

2. The system of claim 1, further comprising an information integration unit receiving data corresponding to entries recorded on the crosslink map from various sources about the genome sequence and transforming the received data into data formats recognized by the crosslink map.

3. The system of claim 1, wherein entries recorded on the crosslink map comprises a name of the genome sequence, a version of the genome sequence, an identifier of the genetic information about the genome sequence, a start position and an end position of the genetic information on the genome sequence, and a length of the genetic information about the genome sequence.

4. The system of claim 1, wherein the location estimation unit determines the location of the target genetic information by assigning a priority to the difference values calculated with respect to genetic information which is contained in a more number in an organism.

5. The system of claim 1, wherein the location estimation unit comprises:

an estimation region setting portion calculating difference values of the start positions and the end positions of genetic information excluded from the reference

group based on the crosslink map and setting an estimation region for the location of the target genetic information on the latest genome sequence based on the calculated difference values; and

a location determining portion determining the location of the target genetic information in the estimation region of the latest genome sequence by a location shift corresponding to the difference values calculated with respect to the reference genetic information.

6. The system of claim 1, wherein the location estimation unit further comprises an updating portion updating the reference group in such a way to calculate difference values of the start positions and the end positions of genetic information which is commonly present on individual versions of the genome sequence and select genetic information in which the calculated difference values are within a predetermined range.

7. A method of designing a probes using heterogeneous genetic information, the method comprising:

creating a crosslink map having records according to the version of a genome sequence;

searching for the identifier and sequence information corresponding to target genetic information among the genetic information about the genome sequence in the crosslink map;

determining a reference group made up of reference genetic information which is contained in more than a predetermined number in an organism;

calculating difference values of the start positions and the end positions of the reference genetic information based on the crosslink map; and

determining the location of the target genetic information on the latest genome sequence by a location shift corresponding to the difference values.

8. The method of claim 7, wherein entries recorded on the crosslink map comprises a name of the genome sequence, a version of the genome sequence, an identifier of the genetic information about the genome sequence, a start position and an end position of the genetic information on the genome sequence, and a length of the genetic information about the genome sequence.

9. The method of claim 7, wherein determining the location of the target genetic information is carried out by assigning a priority to the difference values calculated with respect to genetic information which is contained in a more number in an organism.

10. The method of claim 7, further comprising updating the reference group in such a way to calculate difference values of the start positions and the end positions of genetic information which is commonly present on individual versions of the genome sequence and select genetic information in which the calculated difference values are within a predetermined range.

11. The method of claim 7, wherein determining the location of the target genetic information comprises:

calculating difference values of the start positions and the end positions of genetic information excluded from the reference group based on the crosslink map and setting an estimation region for the location of the target genetic information on the latest genome sequence based on the calculated difference values; and

determining the location of the target genetic information in the estimation region of the latest genome sequence by a location shift corresponding to the difference values calculated with respect to the reference genetic information.

12. A computer readable medium having embodied thereon a computer program for a method of designing a probes using heterogeneous genetic information, the method comprising:

creating a crosslink map having records according to the version of a genome sequence;

searching for the identifier and sequence information corresponding to target genetic information among the genetic information about the genome sequence in the crosslink map;

determining a reference group made up of reference genetic information which is contained in more than a predetermined number in an organism;

calculating difference values of the start positions and the end positions of the reference genetic information based on the crosslink map; and

determining the location of the target genetic information on the latest genome sequence by a location shift corresponding to the difference values.